



#116

SEQUENCE LISTING

<110> Singh, Mohan
Bhalla, Prem
Hui-Ling, Xu
Swoboda, Ines

<120> NOVEL NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> 13334

<140> 09/463,480

<141> 2000-04-07

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 1

gtactcttaa gcatacaaca tgag

24

<210> 2

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 2

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24

<210> 3

<211> 625

<212> DNA

<213> Lilium longiflorum

<220>

<221> CDS

<222> (82)..(468)

<400> 3

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Phe	Glu	Val	Asn	Leu	Ile	Asn	Asn	Leu	Tyr	Cys	Ala	Gln	Ser	Asn	Val
	50					55					60				
Lys	Val	Ser	Cys	Asp	Gly	Leu	His	Thr	Thr	Glu	Pro	Ile	Asp	Pro	His
	65				70					75					80
Ile	Ile	Arg	Pro	Leu	Ser	Asp	Gly	Thr	Asn	Asn	Cys	Leu	Val	Asn	Asn
				85					90					95	
Gly	Ala	Pro	Ile	Ser	His	Ala	Thr	Leu	Val	Ala	Phe	Lys	Tyr	Ala	Trp
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 <213> Lilium longiflorum

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 <222> (49)..(378)

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 Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser Arg Arg Lys Leu Arg Ser
 5 10 15

gag aag gct gca ctc cag ttc tcc gtc agt cgc gtc gaa tac tcc ctc 153
 Glu Lys Ala Ala Leu Gln Phe Ser Val Ser Arg Val Glu Tyr Ser Leu
 20 25 30 35

aag aag ggg cgc tat tgc agg cgc tta ggc gct acg gcc ccc gtc tac 201
 Lys Lys Gly Arg Tyr Cys Arg Arg Leu Gly Ala Thr Ala Pro Val Tyr
 40 45 50

cta gcc gcc gtc ctt gaa aac ctc gtg gcc gaa gtg ttg gac atg gcg 249
 Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp Met Ala
 55 60 65

gcg aac gtg aca gaa gaa aca tcc ccc att gtt atc aaa ccg agg cat 297
 Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys Pro Arg His
 70 75 80

att atg ctt gcc ccc agg aat gat gta gaa gtt gaa caa gct gtt tca 345
 Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln Ala Val Ser
 85 90 95

cgg tgt cac cat ctc ggc atc agg tgt cgt ccc taaaacacgc aaagagctgg 398
 Arg Cys His His Leu Gly Ile Arg Cys Arg Pro
 100 105 110

accgtcgcaa acgccgttcc acctttcagc cggattagtt cttgatattt cattctatca 458
 atcttggtta tgtgactgtg atttttcggtt ttgtgttgaa ctaagccccc taatctggat 518
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 aaaaaaaaaa 587

<210> 6
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 <212> PRT
 <213> Lilium longiflorum

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 35 40 45
 Pro Val Tyr Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu
 50 55 60
 Asp Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys
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 Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln
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 <222> (16)..(348)

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 1 5 10

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 Ala Arg Met Lys His Thr Ala Arg Met Ser Thr Gly Gly Lys Ala Pro
 15 20 25
 cgc aag cag ctc gcc tct aag gct ctt cgc aag gcg cca cca cca ccg 147
 Arg Lys Gln Leu Ala Ser Lys Ala Leu Arg Lys Ala Pro Pro Pro Pro
 30 35 40
 acc aaa gga gtg aag cag ccc acc act acc acc tcc gga aaa tgg cgc 195
 Thr Lys Gly Val Lys Gln Pro Thr Thr Thr Thr Ser Gly Lys Trp Arg
 45 50 55 60
 ttc gcg aga ttt cac agg aaa ctg cca ttc caa ggg ctg gtg agg aaa 243
 Phe Ala Arg Phe His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys
 65 70 75
 atc tgg cag gac ttg aag aca cat ctg cgc ttc aag aac cac tcg gtt 291
 Ile Trp Gln Asp Leu Lys Thr His Leu Arg Phe Lys Asn His Ser Val
 80 85 90
 cct cca ctt gag gag gta act gag gtt tat cct tgc caa act att gga 339
 Pro Pro Leu Glu Glu Val Thr Glu Val Tyr Pro Cys Gln Thr Ile Gly
 95 100 105
 gga tgc tat taggatattg aatttggata atggtttaat tatctgttct 388
 Gly Cys Tyr
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 <212> PRT
 <213> Lilium longiflorum

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 35 40 45
 Lys Gln Pro Thr Thr Thr Thr Ser Gly Lys Trp Arg Phe Ala Arg Phe
 50 55 60
 His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys Ile Trp Gln Asp
 65 70 75 80

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<211> 945
<212> DNA
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tatgctcaaa taactgggtc tttaatgaat agataattaa gttttgtagc aatttcttcc 180
tcaaattgag tatcaacaat tgtagattg ctttggtgat tatatttgat ataattgttt 240
gtaagaatgt gtagtgaaaa gattgtgatt attcatttcg ttgttgagacg aattgttaga 300
gccccatcgc taatgcctta tagtactcga aatatgttgga gaatagaaga tgaaaaatcc 360
cattctttgt agtaggagta aaaatttgct ttttcattat tccattgaat gttaaccact 420
tgccattcat ctgacgggga tggcagagtt ccgaccatct agtgatccgt gggatattga 480
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gggtgctgta gagacagaat ttgaaagttc taacaataaa ccctaattct gaacttgggc 660
ggggctggga ttttactctt aacgtgaaga gaggcaagat gaattgacag cttggaagtc 720
gatccagtat ttgcagcagt cgtgacgaat tggttggaca gttacatcgg tcagagaatg 780
cgttctataa attcccccaa tgcggcagtg aaaatcccat cccatcaaca gaagttttaa 840
gtggaaaccc attccaatag agaagatcga acaaagggtt tttaaacata caaatggggg 900
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<210> 10
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<223> Description of Artificial Sequence:primer

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<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 11
tgtgaaccat acagaagaga acgc

24

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (OTHER THAN US): THE UNIVERSITY OF MELBOURNE
(US ONLY): SINGH Mohan, BHALLA Prem, HUI-LING Xu and
SWOBODA Ines

(ii) TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
THEREFOR

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL
(B) FILING DATE: 24-JUL-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO8233
(B) FILING DATE: 25-JUL-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PP1184
(B) FILING DATE: 31-DEC-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES, DR E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/AF

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777

(B) TELEFAX: +61 3 9254 2770

(C) TELEX: AA 31787

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTACTCTTAA GCATACAACA TGAG

14

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGGCATACT TGAATGCTAC AAGA

14

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 625 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 82..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGGTACTCTT AAGCATACAA C ATG AGG GCG GTG GCG GTT TTC TTT GCT TGC 111
 Met Arg Ala Val Ala Val Phe Phe Ala Cys
 1 5 10

GTT CTC TTC TGT ATG GTT CAC AAA GCC GCA CTT GCG GAT GAT AAA ACG 159
 Val Leu Phe Cys Met Val His Lys Ala Ala Leu Ala Asp Asp Lys Thr
 15 20 25

TGC AAC CCT ACA GAT TTT ATG GTT ACC CAA ACC ATA ACT GGA TTG ACA 207

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Cys	Asn	Pro	Thr	Asp	Phe	Met	Val	Thr	Gln	Thr	Ile	Thr	Gly	Leu	Thr		
			30					35					40				
ATC	GGC	GGT	AAA	CAA	GAG	TTC	GAG	GTC	AAT	TTA	ATA	AAC	AAT	TTG	TAT		255
Ile	Gly	Gly	Lys	Gln	Glu	Phe	Glu	Val	Asn	Leu	Ile	Asn	Asn	Leu	Tyr		
		45					50					55					
TGT	GCA	CAA	TCT	AAT	GTC	AAA	GTT	TCA	TGT	GAC	GGG	CTT	CAT	ACC	ACC		303
Cys	Ala	Gln	Ser	Asn	Val	Lys	Val	Ser	Cys	Asp	Gly	Leu	His	Thr	Thr		
	60					65					70						
GAA	CCA	ATA	GAT	CCT	CAC	ATT	ATC	AGA	CCA	CTT	AGT	GAC	GGA	ACG	AAC		351
Glu	Pro	Ile	Asp	Pro	His	Ile	Ile	Arg	Pro	Leu	Ser	Asp	Gly	Thr	Asn		
	75				80					85					90		
AAC	TGC	CTT	GTC	AAC	AAT	GGA	GCG	CCT	ATT	TCT	CAT	GCT	ACT	CTT	GTA		399
Asn	Cys	Leu	Val	Asn	Asn	Gly	Ala	Pro	Ile	Ser	His	Ala	Thr	Leu	Val		
				95				100						105			
GCA	TTC	AAG	TAT	GCC	TGG	GAT	GTT	CCT	CCA	TCT	TTC	AGC	ATC	ATC	AGC		447
Ala	Phe	Lys	Tyr	Ala	Trp	Asp	Val	Pro	Pro	Ser	Phe	Ser	Ile	Ile	Ser		
		110					115						120				
TCT	GAT	ATA	AAT	TGC	TCC	TAA	GGAGAAA	ATTCTAGTTG	GCAGAGAATA								495
Ser	Asp	Ile	Asn	Cys	Ser	OCH											
	125																
ATCATATAGT	CTTTTTTACT	GAGCTATTTA	ATTTTTTCAA	TTTTCACCAA	TAAGATTATT												555
TTAATGGAAT	GTTAATGTAT	TAGAATTGAA	AAATAAAAAA	AAAAAAAAAA	AAAAAAAAAA												615
AAAAAAAAAA																	625

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Ala	Val	Ala	Val	Phe	Phe	Ala	Cys	Val	Leu	Phe	Cys	Met	Val		
1				5					10					15			
His	Lys	Ala	Ala	Leu	Ala	Asp	Asp	Lys	Thr	Cys	Asn	Pro	Thr	Asp	Phe		
		20						25					30				
Met	Val	Thr	Gln	Thr	Ile	Thr	Gly	Leu	Thr	Ile	Gly	Gly	Lys	Gln	Glu		
		35					40					45					
Phe	Glu	Val	Asn	Leu	Ile	Asn	Asn	Leu	Tyr	Cys	Ala	Gln	Ser	Asn	Val		
	50					55					60						
Lys	Val	Ser	Cys	Asp	Gly	Leu	His	Thr	Thr	Glu	Pro	Ile	Asp	Pro	His		
	65				70				75					80			
Ile	Ile	Arg	Pro	Leu	Ser	Asp	Gly	Thr	Asn	Asn	Cys	Leu	Val	Asn	Asn		
			85						90					95			
Gly	Ala	Pro	Ile	Ser	His	Ala	Thr	Leu	Val	Ala	Phe	Lys	Tyr	Ala	Trp		
		100						105					110				
Asp	Val	Pro	Pro	Ser	Phe	Ser	Ile	Ile	Ser	Ser	Asp	Ile	Asn	Cys	Ser	OCH	

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115

120

125

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAAAGT	TGAA	ACATCT	CCAT	CAA	ACTCT	AGT	CAGATT	TTT	CCC	ACAAG	ATG	ATT	TCA	57					
											Met	Ile	Ser						
											1								
TCG	GCA	AAT	AAC	AAA	GGC	GCC	GGC	ACA	AGC	CGC	CGC	AAG	CTC	CGT	TCT	105			
Ser	Ala	Asn	Asn	Lys	Gly	Ala	Gly	Thr	Ser	Arg	Arg	Lys	Leu	Arg	Ser				
	5					10					15								
GAG	AAG	GCT	GCA	CTC	CAG	TTC	TCC	GTC	AGT	CGC	GTC	GAA	TAC	TCC	CTC	153			
Glu	Lys	Ala	Ala	Leu	Gln	Phe	Ser	Val	Ser	Arg	Val	Glu	Tyr	Ser	Leu				
20					25					30					35				
AAG	AAG	GGG	CGC	TAT	TGC	AGG	CGC	TTA	GGC	GCT	ACG	GCC	CCC	GTC	TAC	201			
Lys	Lys	Gly	Arg	Tyr	Cys	Arg	Arg	Leu	Gly	Ala	Thr	Ala	Pro	Val	Tyr				
			40						45					50					
CTA	GCC	GCC	GTC	CTT	GAA	AAC	CTC	GTG	GCC	GAA	GTG	TTG	GAC	ATG	GCG	249			
Leu	Ala	Ala	Val	Leu	Glu	Asn	Leu	Val	Ala	Glu	Val	Leu	Asp	Met	Ala				
			55					60					65						
GCG	AAC	GTG	ACA	GAA	GAA	ACA	TCC	CCC	ATT	GTT	ATC	AAA	CCG	AGG	CAT	297			
Ala	Asn	Val	Thr	Glu	Glu	Thr	Ser	Pro	Ile	Val	Ile	Lys	Pro	Arg	His				
	70						75					80							
ATT	ATG	CTT	GCC	CCC	AGG	AAT	GAT	GTA	GAA	GTT	GAA	CAA	GCT	GTT	TCA	345			
Ile	Met	Leu	Ala	Pro	Arg	Asn	Asp	Val	Glu	Val	Glu	Gln	Ala	Val	Ser				
	85					90					95								
CGG	TGT	CAC	CAT	CTC	GGC	ATC	AGG	TGT	CGT	CCC	TAAA	ACACGC	AAAG	AGCTGG		398			
Arg	Cys	His	His	Leu	Gly	Ile	Arg	Cys	Arg	Pro									
100					105					110									
ACCG	TCG	C	AA	ACG	CCG	T	TCC	AC	CTT	T	CAGC	CG	GAT	T	AGTT	CTTGATATTT	CATTCTATCA	458	
ATCT	TGG	T	TA	TGT	G	ACT	GTG	AT	TTT	T	CGTT	TT	GTG	T	TGAA	CTAAGCCCCC	TAATCTGGAT	518	
TTCT	CGT	TTT	TT	AT	G	T	TGA	ACT	A	AGT	CT	GTGC	ACT	C	T	TGAAG	TAAAA	AAAA	578
AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	587

(2) INFORMATION FOR SEQ ID NO:6:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Ile Ser Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser Arg Arg Lys
 1           5           10           15
Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe Ser Val Ser Arg Val Glu
          20           25           30
Tyr Ser Leu Lys Lys Gly Arg Tyr Cys Arg Arg Leu Gly Ala Thr Ala
          35           40           45
Pro Val Tyr Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu
          50           55           60
Asp Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys
65           70           75           80
Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln
          85           90           95
Ala Val Ser Arg Cys His His Leu Gly Ile Arg Cys Arg Pro
          100          105          110

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 16..348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GATCCCAAAT CATCA ATG ACG ATC CCC GAA AAG AAA TCC GTC GCT CCG ATG      51
      Met Thr Ile Pro Glu Lys Lys Ser Val Ala Pro Met
          1           5           10
GCC CGT ATG AAG CAT ACA GCC CGC ATG TCT ACC GGC GGT AAG GCT CCA      99
Ala Arg Met Lys His Thr Ala Arg Met Ser Thr Gly Gly Lys Ala Pro
          15           20           25
CGC AAG CAG CTC GCC TCT AAG GCT CTT CGC AAG GCG CCA CCA CCA CCG      147
Arg Lys Gln Leu Ala Ser Lys Ala Leu Arg Lys Ala Pro Pro Pro Pro
          30           35           40
ACC AAA GGA GTG AAG CAG CCC ACC ACT ACC ACC TCC GGA AAA TGG CGC      195
Thr Lys Gly Val Lys Gln Pro Thr Thr Thr Thr Ser Gly Lys Trp Arg
          45           50           55           60
TTC GCG AGA TTT CAC AGG AAA CTG CCA TTC CAA GGG CTG GTG AGG AAA      243
Phe Ala Arg Phe His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys
          65           70           75

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[illegible]

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met 1	Thr	Ile	Pro	Glu 5	Lys	Lys	Ser	Val	Ala 10	Pro	Met	Ala	Arg	Met 15	Lys
His	Thr	Ala	Arg 20	Met	Ser	Thr	Gly	Gly 25	Lys	Ala	Pro	Arg	Lys 30	Gln	Leu
Ala	Ser	Lys 35	Ala	Leu	Arg	Lys	Ala 40	Pro	Pro	Pro	Pro	Thr 45	Lys	Gly	Val
Lys	Gln 50	Pro	Thr	Thr	Thr	Thr 55	Ser	Gly	Lys	Trp	Arg 60	Phe	Ala	Arg	Phe
His 65	Arg	Lys	Leu	Pro	Phe 70	Gln	Gly	Leu	Val	Arg 75	Lys	Ile	Trp	Gln	Asp 80
Leu	Lys	Thr	His	Leu 85	Arg	Phe	Lys	Asn	His 90	Ser	Val	Pro	Pro	Leu 95	Glu
Glu	Val	Thr	Glu 100	Val	Tyr	Pro	Cys	Gln 105	Thr	Ile	Gly	Gly	Cys 110	Tyr	

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAGGGTGTGTT GGAATTAGGT TTGCCTAGGG TTTGCCTAGG TTTAGAGAAA TAGTCAAAAT	60
TGTCCTATTC TATAGGCATG ATTTAGTAGT GAGTTAAATTA TCCTATAATT TCTCTTCTTG	120
TATGCTCAAA TAACTGGTTC TTTAATGAAT AGATAATTAA GTTTTGTAGC AATTTCTTCC	180
TCAAATTGAG TATCAACAAT TGTTAGATTG CTTTGGTGAT TATATTTGAT ATAATTGTTT	240
GTAAGAATGT GTAGTGAAAA GATTGTGATT ATTCATTTTCG TTGTTGGACG AATTGTTAGA	300
GCCCCATCGC TAATGCCTTA TAGTACTCGA AATATGTTGG GAATAGAAGA TGAAAAATCC	360
CATTCTTTGT AGTAGGAGTA AAAATTTGTC TTTTCATTAT TCCATTGAAT GTTAACCACT	420
TGCCATTCAT CTGACGGGGA TGGCAGAGTT CCGACCATCT AGTGATCCGT GGGATATTGA	480
TTTTGGTGTG TCAATGAAAT TGTGAGAAGG GGCTTCTGGG AGAGAAAAGC CCTCTTGCCT	540
CTGATATGAA CACTGAGGCT GATTATGTTA ACGGATGGAG ATTTATCAGT GGCTGAATTT	600
GGGTGCTGTA GAGACAGAAT TTGAAAGTTC TAACAATAAA CCCTAATTCT GAACTTGGGC	660
GGGGCTGGGA TTTTACTCTT AACGTGAAGA GAGGCAAGAT GAATTGACAG CTTGGAAGTC	720
GATCCAGTAT TTGCAGCAGT CGTGACGAAT TGGTTGGACA GTTACATCGG TCAGAGAATG	780
CGTTCTATAA ATTCCCCCAA TGCGGCAGTG AAAATCCCAT CCCATCAACA GAAGTTTTAA	840
GTGGAAACCC ATTCCAATAG AGAAGATCGA ACAAAGGGTA TTAAACATA CAAATGGGGG	900
CAGTGGTGTG TCTTTTGTGCT TCGTTTCTCT TCTGTATGGT TCACA	945

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGCATACT TGAATGCTAC AAGA

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

- 35 -

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTGAACCAT ACAGAAGAGA ACGC

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